

AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application:

LISTING OF CLAIMS:

1-4. (cancelled).

5. (currently amended): A method for detecting a SARS coronavirus in a sample, comprising: (1) amplifying amplification of a target nucleic acid region of the SARS coronavirus consisting of the nucleotide sequence of SEQ ID NO:1 using a first an oligonucleotide primer comprising at least 15 contiguous nucleotides of SEQ ID NO:17; or a nucleotide sequence entirely complementary thereto to said first oligonucleotide primer, a second oligonucleotide primer comprising at least 15 contiguous nucleotides of SEQ ID NO:18; or a nucleotide sequence entirely complimentary thereto complementary to said second oligonucleotide primer, a third oligonucleotide primer comprising at least 15 contiguous nucleotides of SEQ ID NO:10; or a nucleotide sequence entirely complimentary thereto complementary to said third oligonucleotide primer, and a fourth oligonucleotide primer comprising at least 15 contiguous nucleotides of SEQ ID NO:19; or a nucleotide sequence entirely complimentary thereto complementary to said fourth oligonucleotide primer; (2) detecting a product of said target nucleic acid amplification, and wherein the detection of said product indicates that said sample contains a SARS coronavirus.

6. (canceled).

7. (currently amended): A-The method of Claim 5, wherein said sample is obtained from an animal and wherein detection of a SARS coronavirus in said sample indicates that said animal is afflicted with for diagnosing severe acute respiratory syndrome (SARS)-comprising diagnosing infection with the SARS coronavirus by detecting amplification of a target nucleic acid region of the SARS coronavirus using the oligonucleotide primers according to claim 5.

8 - 11. (canceled).

12. (currently amended): The method of claim 5, wherein said first, second, third and fourth primers comprise a nucleotide sequence of SEQ ID NO:1 selected from the following nucleotide sequences (a) to (d), provided that the an F3c, the an F2c, and the an F1c regions region are-is selected from the 3'-terminus and the an R3, the an R2, and the an R1 regions region are-is selected from the 5'-terminus of the target nucleic acid of the SARS coronavirus, and nucleotide sequences entirely complementary thereto to each of said primers are determined to be F3, F2, and F1 and R3c, R2c, and R1c, respectively:

- (a) a nucleotide sequence having the an F2 region and the an F1c region of the target nucleic acid at the 3'-terminus and the 5'-terminus, respectively;
- (b) a nucleotide sequence having the an F3 region of the target nucleic acid;
- (c) a nucleotide sequence having the an R2 region and the an R1c region of the target nucleic acid at the 3'-terminus and the 5'-terminus, respectively; and
- (d) a nucleotide sequence having the an R3 region of the target nucleic acid.

13 - 20. (cancelled).

21. (currently amended): The method according to claim 5, further comprising a fifth oligonucleotide primer comprising at least 15 contiguous nucleotides of SEQ ID NO:22, or a nucleotide sequence entirely complementary thereto~~complementary to said fifth oligonucleotide primer~~, and a sixth oligonucleotide primer comprising at least 15 contiguous nucleotides of SEQ ID NO:23, or a nucleotide sequence entirely complementary eomplimentary thereteto~~complementary to said sixth oligonucleotide primer~~.